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# Fig. 1a

GAATTCGCGG CCGCCTCTTG CCGTCCCAGA GTGGAGTGA AGGTCTGGAG CTTTGGGAGG	60
AGACGGGGAG GACAGACTGG AGGCGTGTC CTCCCGGATT TTCTTTTTCG TCGAGCCCT	120
CGCGCGCGCG TACAGTCATC CCGCTGGTCT GACGATTGTG GAGAGCGGT GGAGAGGCTT	180
CATCCATCCC ACCCGGTCGT CGCCGGGGAT TGGGTCCCA GCGACACCTC CCCGGGAGAA	240
GCAGTGCCCA GGAAGTTTTC TGAAGCCGGG GAAGCTGTGC AGCCGAAGCC GCCGCCGCGC	300
CGGAGCCCGG GACACCGGCC ACCCTCCGCG CCACCCACCC TCGCTTTCTC CGGCTTCCTC	360
TGGCCAGGC GCCGCGCGGA CCCGGCAGCT GTCTGCGCAC GCCGAGCTCC ACGGTGAAAA	420
AAAAAGTGAA GGTGTAAAAG CAGCACAAGT GCAATAAGAG ATATTTCCTC AAATTTGCCT	480
CAAG ATG GAA ACC CTT TGC CTC AGG GCA TCC TTT TGG CTG GCA CTG GTT	529
Met Glu Thr Leu Cys Leu Arg Ala Ser Phe Trp Leu Ala Leu Val	
-20 -15 -10	577
GGA TGT GTA ATC AGT GAT AAT CCT GAG AGA TAC AGC ACA AAT CTA AGC	
Gly Cys Val Ile Ser Asp Asn Pro Glu Arg Tyr Ser Thr Asn Leu Ser	
-5 -1 1 5 10	
AAT CAT GTG GAT GAT TTC ACC ACT TTT CGT GGC ACA GAG CTC AGC TTC	625
Asn His Val Asp Asp Phe Thr Thr Phe Arg Gly Thr Glu Leu Ser Phe	
15 20 25	
CTG GTT ACC ACT CAT CAA CCC ACT AAT TTG GTC CTA CCC AGC AAT GGC	673
Leu Val Thr Thr His Gln Pro Thr Asn Leu Val Leu Pro Ser Asn Gly	
30 35 40	
TCA ATG CAC AAC TAT TGC CCA CAG CAG ACT AAA ATT ACT TCA GCT TTC	721
Ser Met His Asn Tyr Cys Pro Gln Gln Thr Lys Ile Thr Ser Ala Phe	
45 50 55	
AAA TAC ATT AAC ACT GTG ATA TCT TGT ACT ATT TTC ATC GTG GGA ATG	769
Lys Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met	
60 65 70 75	

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Fig. 1b

GTG GGG AAT GCA ACT CTG CTC AGG ATC ATT TAC CAG AAC AAA TGT ATG	817
Val Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met	
80 85 90	
AGG AAT GGC CCC AAC GCG CTG ATA GCC AGT CTT GCC CTT GGA GAC CTT	865
Arg Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu	
95 100 105	
ATC TAT GTG GTC ATT GAT CTC CCT ATC AAT GTA TTT AAG CTG CTG GCT	913
Ile Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala	
110 115 120	
GGG CGC TGG CCT TTT GAT CAC AAT GAC TTT GGC GTA TTT CTT TGC AAG	961
Gly Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys	
125 130 135	
CTG TTC CCC TTT TTG CAG AAG TCC TCG GTG GGG ATC ACC GTC CTC AAC	1009
Leu Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn	
140 145 150 155	
CTC TGC GCT CTT AGT GTT GAC AGG TAC AGA GCA GTT GCC TCC TGG AGT	1057
Leu Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser	
160 165 170	
CGT GTT CAG GGA ATT GGG ATT CCT TTG GTA ACT GCC ATT GAA ATT GTC	1105
Arg Val Gln Gly Ile Gly Ile Pro Leu Val Thr Ala Ile Glu Ile Val	
175 180 185	
TCC ATC TGG ATC CTG TCC TTT ATC CTG GCC ATT CCT GAA GCG ATT GGC	1153
Ser Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly	
190 195 200	
TTC GTC ATG GTA CCC TTT GAA TAT AGG GGT GAA CAG CAT AAA ACC TGT	1201
Phe Val Met Val Pro Phe Glu Tyr Arg Gly Glu Gln His Lys Thr Cys	
205 210 215	

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# Fig. 1c

ATG CTC AAT GCC ACA TCA AAA TTC ATG GAG TTC TAC CAA GAT GTA AAG	1249
Met Leu Asn Ala Thr Ser Lys Phe Met Glu Phe Tyr Gln Asp Val Lys	
220 225 230 235	
GAC TGG TGG CTC TTC GGG TTC TAT TTC TGT ATG CCC TTG GTG TGC ACT	1297
Asp Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr	
240 245 250	
GCG ATC TTC TAC ACC CTC ATG ACT TGT GAG ATG TTG AAC AGA AGG AAT	1345
Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Arg Asn	
225 260 265	
GGC AGC TTG AGA ATT GCC CTC AGT GAA CAT CTT AAG CAG CGT CGA GAA	1393
Gly Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln Arg Arg Glu	
270 275 280	
GTG GCA AAA ACA GTT TTC TGC TTG GTT GTA ATT TTT GCT CTT TGC TGG	1441
Val Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp	
285 290 295	
TTC CCT CTT CAC TTA AGC CGT ATA TTG AAG AAA ACT GTG TAT AAC GAA	1489
Phe Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val Tyr Asp Glu	
300 305 310 315	
ATG GAC AAG AAC CGA TGT GAA TTA CTT AGT TTC TTA CTG CTC ATG GAT	1537
Met Asp Lys Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Leu Met Asp	
320 325 330	
TAC ATC GGT ATT AAC TTG GCA ACC ATG AAT TCA TGT ATA AAC CCC ATA	1585
Tyr Ile Gyr Ile Asn Leu Ala Thr Met Asn Ser Cys Lie Asn Pro Ile	
335 340 345	
GCT CTG TAT TTT GTG AGC AAG AAA TTT AAA AAT TGT TTC CAG TCA TGC	1633
Ala Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser Cys	
350 355 360	

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Fig. 1d

CTC TGC TGC TGC TGT TAC CAG TCC AAA AGT CTG ATG ACC TCG GTC CCC	1681
Leu Cys Cys Cys Cys Tyr Gln Ser Lys Ser Leu Met Thr Ser Val Pro	
365 370 375	
ATG AAC GGA ACA AGC ATC CAG TGG AAG AAC CAC GAT CAA AAC AAC CAC	1729
Met Asn Gly Thr Ser Ile Gln Trp Lys Asn His Asp Gln Asn Asn His	
380 385 390 395	
AAC ACA GAC CGG AGC AGC CAT AAG GAC AGC ATG AAC TGACCACCCT	1775
Asn Thr Asp Arg Ser Ser His Lys Asp Ser Met Asn	
400 405	
TAGAAGCACT CCTCGGTACT CCCATAATCC TCTCGGAGAA AAAAATCACA AGGCAACTGT	1835
GA CTCCGGGA ATCTCTTCTC TGATCCTTCT TCCTTAATTC ACTCCACAC CCAAGAAGAA	1895
ATGCTTTCCA AAACCGCAAG GTAGACTGGT TTATCCACCC ACAACATCTA CGAATCGTAC	1955
TTCTTTAATT GATCTAATTT ACATATTCTG CGTGTGTAT TCAGCACTAA AAAATGGTGG	2015
GAGCTGGGGG AGAATGAAGA CTGTAAATG AAACCAGAAG GATATTTACT ACTTTTGCAT	2075
GAAAATAGAG CTTTCAAGTA CATGGCTAGC TTTTATGGCA GTTCTGGTGA ATGTTCAATG	2135
GGAAGTGGTC ACCATGAAAC TTTAGAGATT AACGACAAGA TTTTCTACTT TTTTAAAGTG	2195
ATTTTTTGTG CTTCAGCCAA ACACAATATG GGCTCAGGTC ACTTTTATTT GAAATGTCAT	2255
TTGGTGCCAG TATTTTTTAA CTGCATAATA GCCTAACATG ATTATTTGAA CTTATTTACA	2315
CATAGTTTGA AAAAAAAAG ACAAAAATAG TATTCAGGTG AGCAATTAGA TTAGTATTTT	2375
CCACGTCACT ATTTATTTTT TTTAAACACA AATTCTAAAG CTACAACAAA TACTACAGGC	2435
CCTTAAAGCA CAGTCTGATG ACACATTTGG CAGTTTAATA GATGTTACTC AAAGAATTTT	2495
TTAAGAACTG TATTTTATTT TTTAAATGGT GTTTTATTAC AAGGGACCTT GAACATGTTT	2555
TGTATGTAA ATTCAAAAGT AATGCTTCAA TCAGATAGTT CTTTTTCACA AGTTCAATAC	2615
TGTTTTTCAT GTAAATTTTG TATGAAAAAT CAATGTCAAG TACCAAAATG TTAATGTATG	2675
TGTCATTTAA CTCTGCCTGA GACTTTCAGT GCACTGTATA TAGAAGTCTA AAACACACCT	2735
AAGAGAAAAA GATCGAATTT TTCAGATGAT TCGGAAATTT TCATTCAAGT ATTTGTAATA	2795

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Fig. 1e

GTGACATATA TATGTATATA CATATCACCT CCTATTCTCT TAATTTTTGT TAAAATGTTA 2855  
ACTGGCAGTA AGTCTTTTTT GATCATTCCC TTTTCCATAT AGGAAACATA ATTTTGAAGT 2915  
GGCCAGATGA GTTTATCATG TCAGTGAAAA ATAATTACCC ACAAATGCCA CCAGTAACTT 2975  
AACGATTCTT CACTTCTTGG GGTTTTCAGT ATGAACCTAA CTCCCCACCC CAACATCTCC 3035  
CTCCACATT GTCACCATT CAAAGGGCCC ACAGTGACTT TTGCTGGGCA TTTTCCAGA 3095  
TGTTTACAGA CTGTGAGTAC AGCAGAAAAT CTTTACTAC TGTGTGTGTG TATATATATA 3155  
AACAATTGTA AATTTCTTTT AGCCCATTTT TCTAGACTGT CTCTGTGGAA TATATTGTG 3215  
TGTGTGATAT ATGCATGTGT GTGATGGTAT GTATGGATT AATCTAATCT AATAATTGTG 3275  
CCCCGCAGTT GTGCCAAAGT GCATAGTCTG AGCTAAAATC TAGGTGATTG TTCATCATGA 3335  
CACCTGCCT CAGTCCATT TAACCTGTAG CAACCTTCTG CATTATAAA TCTTGTAATC 3395  
ATGTTACCAT TACAAATGGG ATATAAGAGG CAGCGTGAAA GCAGATGAGC TGTGGACTAG 3455  
CAATATAGGG TTTTGTGGG TTGGTTGGT TGATAAAGCA GTATTGGGG TCATATTGTT 3515  
TCCTGTGCTG GAGCAAAAGT CATTACACTT TGAAGTATTA TATTGTTCTT ATCTCAATT 3575  
CAATGTGGTG ATGAAATTGC CAGGTTGTCT GATATTTCTT TCAGACTTCG CCAGACAGAT 3635  
TGCTGATAAT AAATTAGGTA AGATAATTG TTGGGCCATA TTTTAGGACA GGTAAAATAA 3695  
CATCAGGTT CAGTTGCTTG AATTGCAAGG CTAAGAAGTA CTGCCCTTTT GTGTGTTAGC 3755  
AGTCAAATCT ATTATTCCAC TGGCGCATCA TATGCAGTGA TATATGCCTA TAATATAAGC 3815  
CATAGGTTCA CACCATTTTG TTTAGACAAT TGTCTTTTTT TCAAGATGCT TTGTTTCTT 3875  
CATATGAAAA AAATGCATT TATAAATTCA GAAAGTCATA GATTTCTGAA GCGTCAACG 3935  
TGCATTTTAT TTATGGACTG GTAAGTAACT GTGGTTTACT AGCAGGAATA TTTCCAATT 3995  
CTACCTTTAC TACATCTTTT CAACAAGTAA CTTTGTAGAA ATGAGCCAGA AGCCAAGGCC 4055  
CTGAGTTGGC AGTGGCCCAT AAGTGTAAAA TAAAAGTTTA CAGAAACCTT 4105

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Fig. 2a

GAGACATTCC GGTGGGGGAC TCTGGCCAGC CCGAGCAACG TGGATCCTGA GAGCACTCCC 60  
AGGTAGGCAT TTGCCCCGGT GGGACGCCTT GCCAGACCAG TGTGTGGCAG GCCCCCGTGG 120  
AGGATCAACA CAGTGGCTGA ACACTGGGAA GGAAGTGGTA CTTGGAGTCT GGACATCTGA 180  
AACTTGGCTC TGAAACTGCG GAGCGGCCAC CCGACGCCTT CTGGAGCAGG TAGCAGC 237  
ATG CAG CCG CCT CCA AGT CTG TGC GGA CGC GCC CTG GTT GCG CTG GTT 285  
Met Gln Pro Pro Pro Ser Leu Cys Gly Arg Ala Leu Val Ala Leu Val  
1 5 10 15  
CTT GCC TGC GGC CTG TCG CGG ATC TGG GGA GAG GAG AGA GGC TTC CCG 333  
Leu Ala Cys Gly Leu Ser Arg Ile Trp Gly Glu Glu Arg Gly Phe Pro  
20 25 30  
CCT GAC AGG GCC ACT CCG CTT TTG CAA ACC GCA GAG ATA ATG ACG CCA 381  
Pro Asp Arg Ala Thr Pro Leu Leu Gln Thr Ala Glu Ile Met Thr Pro  
35 40 45  
CCC ACT AAG ACC TTA TGG CCC AAG GGT TCC AAC GCC AGT CTG GCG CGG 429  
Pro Thr Lys Thr Leu Trp Pro Lys Gly Ser Asn Ala Ser Leu Ala Arg  
50 55 60  
TCG TTG GCA CCT GCG GAG GTG CCT AAA GGA GAC AGG ACG GCA GGA TCT 477  
Ser Leu Ala Pro Ala Glu Val Pro Lys Gly Asp Arg Thr Ala Gly Ser  
65 70 75 80  
CCG CCA CGC ACC ATC TCC CCT CCC CCG TGC CAA GGA CCC ATC GAG ATC 525  
Pro Pro Arg Thr Ile Ser Pro Pro Pro Cys Gln Gly Pro Ile Glu Ile  
85 90 95  
AAG GAG ACT TTC AAA TAC ATC AAC ACG CTT GTG TCC TGC CTT GTG TTC 573  
Lys Glu Thr Phe Lys Tyr Ile Asn Thr Val Val Ser Cys Leu Val Phe  
100 105 110

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Fig. 2b

GTG CTG GGG ATC ATC GGG AAC TCC ACA CTT CTG AGA ATT ATC TAC AAG	621
Val Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lrs	
115 120 125	
AAC AAG TGC ATG CGA AAC GGT CCC AAT ATC TTG ATC GCC AGC TTG GCT	669
Asn Lys Gys Met Arg Asn Gly Pro Asn Ile Leu Ile Ala Ser Leu Ala	
130 135 140	
CTG GGA GAC CTG CTG CAC ATC GTC ATT GAC ATC CCT ATC AAT GTC TAC	717
Leu Gly Asp Leu Leu His Ile Val Ile Asp Ile Pro Ile Asn Val Tyr	
145 150 155 160	
AAG CTG CTG GCA GAG GAC TGG CCA TTT GGA GCT GAG ATG TGT AAG CTG	765
Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly Ala Glu Met Cys Lys Leu	
165 170 175	
GTG CCT TTC ATA CAG AAA GCC TCC GTG GGA ATC ACT GTG CTG AGT CTA	813
Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile Thr Val Leu Ser Leu	
180 185 190	
TGT GCT CTG AGT ATT GAC AGA TAT CGA GCT GTT GCT TCT TGG AGT AGA	861
Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg	
195 200 205	
ATT AAA GGA ATT GGG GTT CCA AAA TGG ACA GCA GTA GAA ATT GTT TTG	909
Ile Lys Gly Ile Gly Val Pro Lys Trp Thr Ala Val Glu Ile Val Leu	
210 215 220	
ATT TGG GTG GTC TCT GTG GTT CTG GCT GTC CCT GAA GCC ATA GGT TTT	957
Ile Trp Val Val Ser Val Val Leu Ala Val Pro Glu Ala Ile Gly Phe	
225 230 235 240	
GAT ATA ATT ACG ATG GAC TAC AAA GGA AGT TAT CTG CGA ATC TGC TTG	1005
Asp Ile Ile Thr Met Asp Tyr Lys Gly Ser Tyr Leu Arg Ile Cys Leu	
245 250 255	

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Fig. 2c

CTT CAT CCC GTT CAG AAG ACA GCT TTC ATG CAG TTT TAC AAG ACA GCA 1053  
Leu His Pro Val Gln Lys Thr Ala Phe Met Gln Phe Tyr Lys Thr Ala  
260 265 270

AAA GAT TGG TGG CTG TTC AGT TTC TAT<sub>V</sub> TTC TGC TTG CCA TTG GCC ATC 1101  
Lys Asp Tyr Trp Leu Phe Ser Phe Tyr Phe Cys Leu Pro Leu Ala Ile  
275 280 285

ACT GCA TTT TTT TAT ACA CTA ATG ACC TGT GAA ATG TTG AGA AAG AAA 1149  
Thr Ala Phe Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Arg Lys Lys  
290 295 300

AGT GGC ATG CAG ATT GCT TTA AAT GAT CAC CTA AAG CAG AGA CGG GAA 1197  
Ser Gly Met Gln Ile Ala Leu Asn Asp His Leu Lys Gln Arg Arg Glu  
305 310 315 320

GTG GCC AAA ACC GTC TTT TGC CTG GTC CTT GTC TTT GCC CTC TGC TGG 1245  
Val Ala Lys Thr Val Phe Cys Leu Val Leu Val Phe Ala Leu Cys Trp  
325 330 335

CTT CCC CTT CAC<sub>VI</sub> CTC AGC AGG ATT CTG AAG CTC ACT GTT TAT AAT CAG 1293  
Leu Pro Leu His Leu Ser Arg Ile Leu Lys Leu Thr Leu Tyr Asp Gln  
340 345 350

AAT GAT CCC AAT AGA TGT GAA CTT TTG AGC TTT CTG TTG GTA TTG GAC 1341  
Asn Asp Pro Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Val Leu Asp  
355 360 365

TAT ATT GGT ATG AAC<sub>VII</sub> ATG GCT TCA CTG AAT TCC TGC ATT AAC CCA ATT 1389  
Tyr Ile Gyr Ile Asn Met Ala Ser Leu Asn Ser Cys Ile Asn Pro Ile  
370 375 380

GCT CTG TAT TTC GTG AGC AAA AGA TTC AAA AAC TGC TTT AAG TCA TGC 1437  
Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys Asn Cys Phe Lys Ser Cys  
385 390 395 400

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T0930 2572600



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## Fig. 2d

TTA TGC TGC TGG TGC CAG TCA TTT GAA GAA AAA CAG TCC TTG GAG GAA	1485
Leu Cys Cys Trp Cys Gln Ser Phe Glu Glu Lys Gln Ser Leu Glu Glu	
405 410 415	
AAG CAG TCG TGC TTA AAG TTC AAA GCT AAT GAT CAC GGA TAT GAC AAC	1533
Lys Gln Ser Cys Leu Lys Phe Lys Ala Asn Asp His Gly Tyr Asp Asn	
420 425 430	
TTC CGT TCC AGT AAT AAA TAC AGC TCA TCT TGAAAGAAGA ACTATTCAT	1583
Phe Arg Ser Ser Asn Lys Tyr Ser Ser Ser	
435 440	
GTATTTCAAT TTCTTTATAT TGGACGGAAG TCATTA <sup>•</sup> AAAC AAAATGAAAC ATTTGCCAAA	1643
ACAAAACAAA AACTATGTA TTTGCACAGC ACACTAT <sup>•</sup> TAA AATATTAAGT GTAATTATTT	1703
TAACACTC <sup>•</sup> CAC AGCTACATAT GACATTTTAT GAGCTGTTT CGGCATGGAA AGAAAATCAG	1763
AGGGAATTAA GAAAGCCTCG TCGTGAAAGC ACTTAATTTT TTACAGTTAG CACTTCAACA	1823
TAGCTCTTAA CAACTTCCAG GATATTCACA CAACACTTAG GCTTAAAAAT GAGCTCACTC	1883
AGAATTTCTA TTCTTTCTAA AAAGAGATTT ATTTTAAAT CAATGGGACT CTGATATAAA	1943
GGAAGAATAA GTCACTGTAA AACAGAACTT TTAAATGAAG CTAAATTAC TCAATTTAAA	2003
ATTTTAAAT CCTTTAAAC AACTTTTCAA TTAATATTAT CACACTATTA TCAGATTGTA	2063
ATTAGATGCA AATGAGAGAG CAGTTTAGTT GTTGCATTTT TCGGACACTG GAAAGATTTA	2123
AATGATCAGG AGGGAGTAAC AGAAAGAGCA AGGCTGTTTT TGAAATTCAT TACACTTTCA	2183
CTAGAAGCCC AAACCTCAGC ATTCTGCAAT ATGTAACCAA CATGTCACAA ACAAGCAGCA	2243
TGTAACAGAC TGGCACATGT GCCAGCTGAA TT <sup>•</sup> TAAAATAT AATACTTTTA AAAAGAAAAT	2303
TATTACATCC TTTACATTCA GTTAAGATCA AACCTCACAA AGAGAAATAG AATGTTTGAA	2363
AGGCTATCCC AAAAGACTTT TTTGAATCTG TCATTCACAT ACCCTGTGAA GACAATACTA	2423
TCTACAATTT TTTCAGGATT ATTAAATCT TCTTTTTTCA CTATCGTAGC TTAAACTCTG	2483
TTTGGTTTTG TCATCTGTAA ATACTTACCT ACATACACTG CATGTAGATG ATTAAATGAG	2543
GGCAGGCCCT GTGCTCATAG CTTTACGATG GAGAGATGCC AGTGACCTCA TA <sup>•</sup> TA <sup>•</sup> AA <sup>•</sup> GAC	2603
TGTGA <sup>•</sup> ACTGC CTGGTGCAGT GTCCACATGA CAAAGGGGCA GGTAGCACCC TCTCTCACCC	2663

Fig. 2e

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ATGCTGTGGT TAAAATGGTT TCTAGCATAT GTATAATGCT ATAGTTAAAA TACTATTTTT 2723  
CAAAATCATA CAGATTAGTA CATTTAACAG CTACCTGTAA AGCTTATTAC TAATTTTTGT 2783  
ATTATTTTTG TAAATAGCCA ATAGAAAAGT TTGCTTGACA TGGTGCTTTT CTTTCATCTA 2843  
GAGGCAAAAC TGCTTTTTGA GACCGTAAGA ACCTCTTAGC TTTGTGCGTT CCTGCCTAAT 2903  
TTTTATATCT TCTAAGCAAA GTGCCTTAGG ATAGCTTGGG ATGAGATGTG TGTGAAAGTA 2963  
TGTACAAGAG AAAACGGAAG AGAGAGGAAA TGAGGTGGGG TTGGAGGAAA CCCATGGGGA 3023  
CAGATTCCCA TTCTTAGCCT AACGTTGCTC ATTGCCTCGT CACATCAATG CAAAAGGTCC 3083  
TGATTTTGTT CCAGCAAAAC ACAGTGCAAT GTTCTCAGAG TGACTTTCGA AATAAATTGG 3143  
GCCAAGAGC TTTAACTCGG TCTTAAAATA TGCCCAAATT TTTACTTTGT TTTTCTTTTA 3203  
ATAGGCTGGG CCACATGTTG GAAATAAGCT AGTAATGTTG TTTTCTGTCA ATATTGAATG 3263  
TGATGGTACA GTAAACCAAA ACCCAACAAT GTGGCCAGAA AGAAAGAGCA ATAATAATTA 3323  
ATTACACAC CATATGGATT CTATTTATAA ATCACCACAA AACTTGTTCT TTAATTTTCA 3383  
CCCAATCACT TTTTCAGAGG CCGTTATCA TAGAAGTCAT TTAGACTCT CAATTTTAAA 3443  
TTAATTTTGA ATCACTAATA TTTTCACAGT TTATTAATAT ATTTAATTC TATTTAAATT 3503  
TTAGATTATT TTTATTACCA TGTACTGAAT TTTTACATCC TGATACCCTT TCCTTCTCCA 3563  
TGTCAGTATC ATGTTCTCTA ATTATCTTGC CAAATTTTGA AACTACACAC AAAAAGCATA 3623  
CTTGCATTAT TTATAATAAA ATTGCATTCA GTGGCTTTTT AAAAAAATG TTTGATTCAA 3683  
AACTTTAACA TACTGATAAG TAAGAAACAA TTATAATTC TTTACATACT CAAAACCAAG 3743  
ATAGAAAAAG GTGCTATCGT TCAACTTCAA AACATGTTTC CTAGTATTAA GGACTTTAAT 3803  
ATAGCAACAG ACAAATTAT TGTTAACATG GATGTTACAG CTCAAAAGAT TTATAAAAGA 3863  
TTTTAACCTA TTTTCTCCCT TATTATCCAC TGCTAATGTG GATGTATGTT CAAACACCTT 3923  
TTAGATTGA TAGCTTACAT ATGGCCAAAG GAATACAGTT TATAGCAAAA CATGGGTATG 3983  
CTGTAGCTAA CTTTATAAAA GTGTAATATA ACAATGTAAA AAATTATATA TCTGGGAGGA 4043  
TTTTTTGGTT GCCTAAAGTG GCTATAGTTA CTGATTTTTT ATTATGTAAG CAAAACCAAT 4103  
AAAAATTTAA GTTTTTTTAA CAACTACCTT ATTTTTCCT GTACAGACAC TAATTCATTA 4163  
AATACTAATT GATTGTTTAA AAGAAATATA AATGTGACAA GTGGACATTA TTTATGTTAA 4223  
ATATACAATT ATCAAGCAAG TATGAAGTTA TTCAATTA ATGCCACATT TCTGGTCTCT 4283  
GGGAAAAAAA AAAAAAAA 4301

00934457-001504  
FIG. 2e

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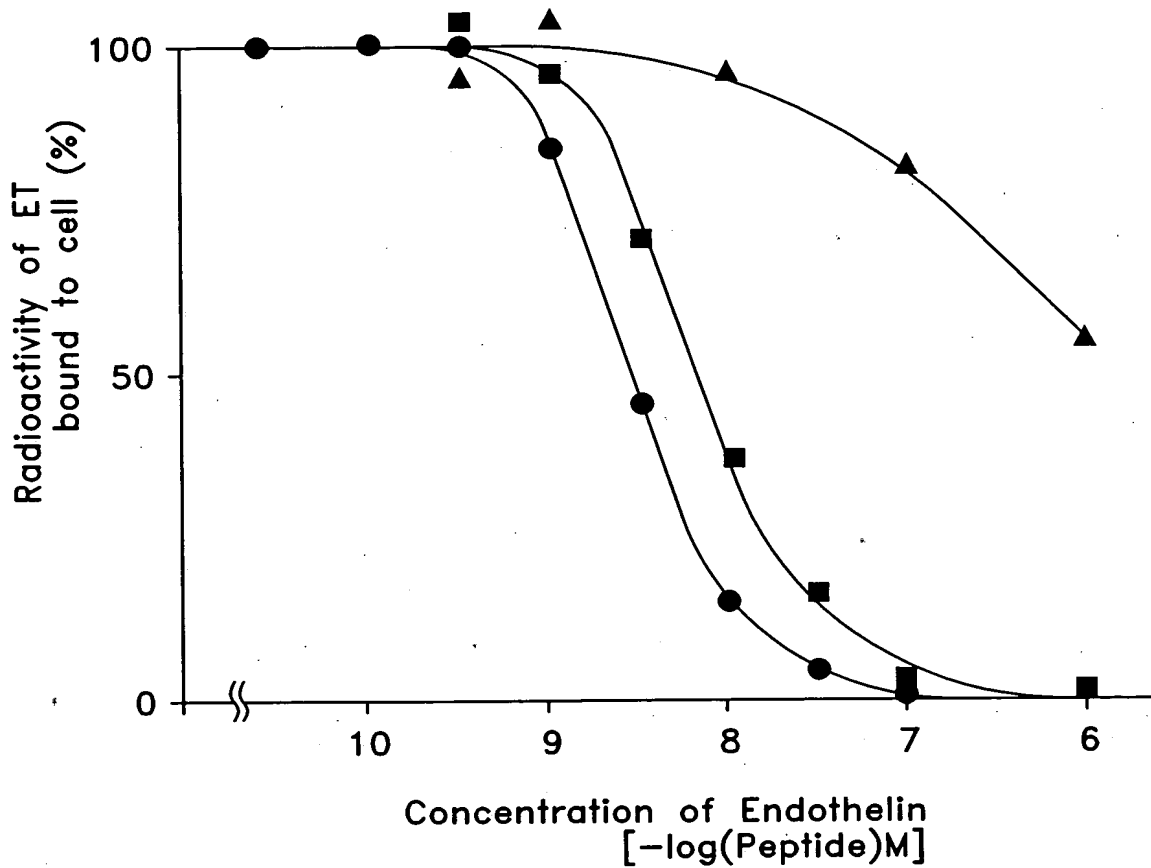


Fig. 3

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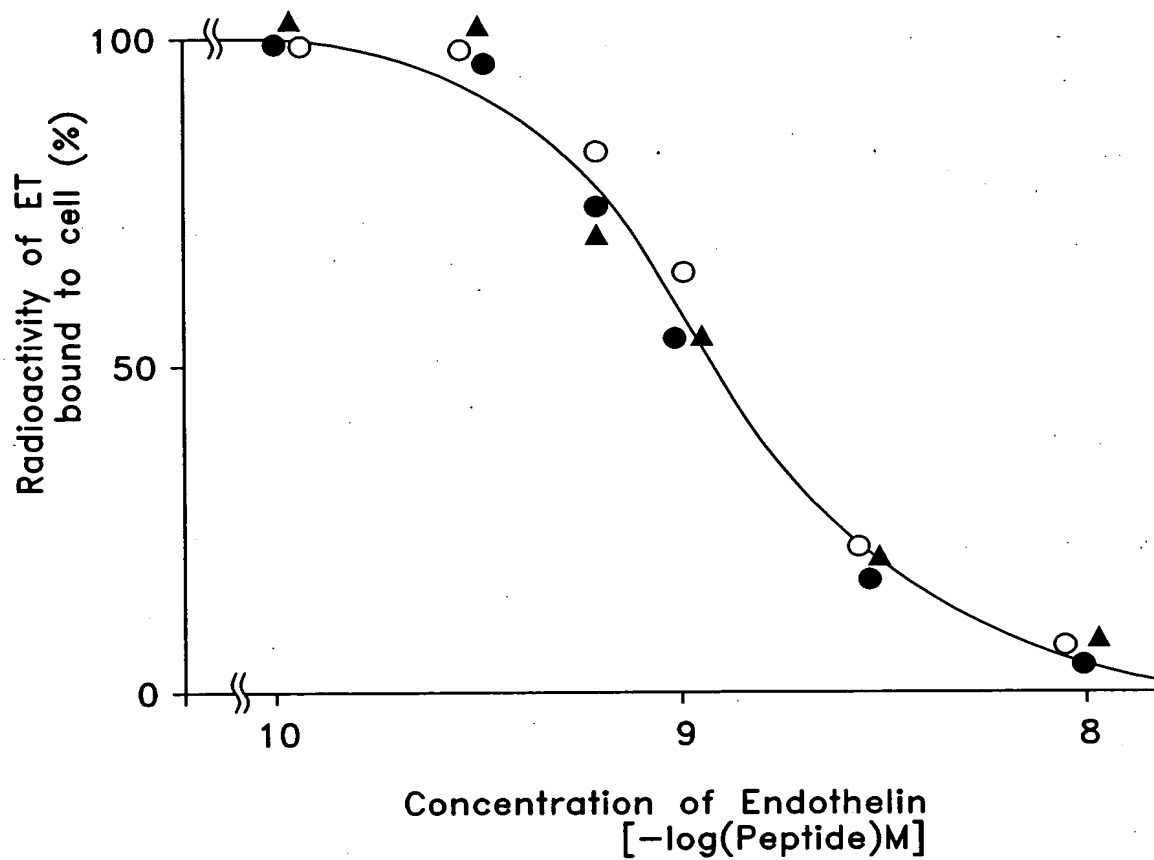


Fig. 4

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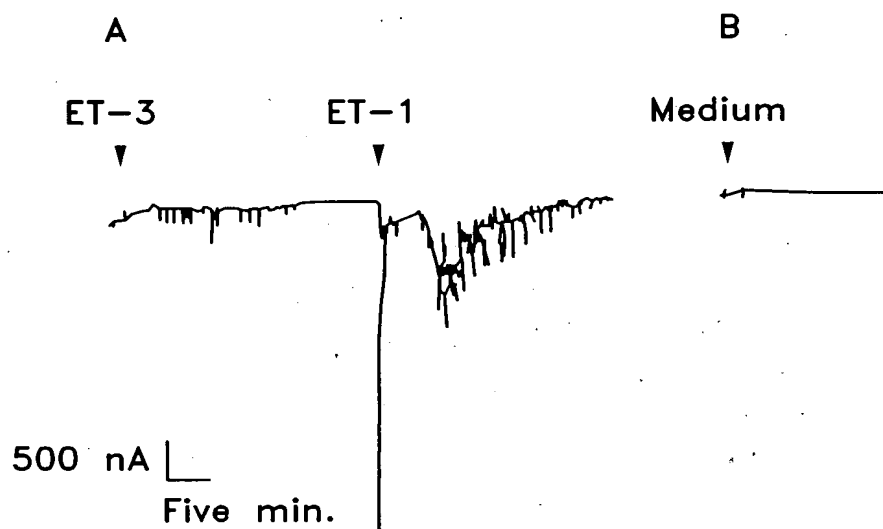


Fig. 5

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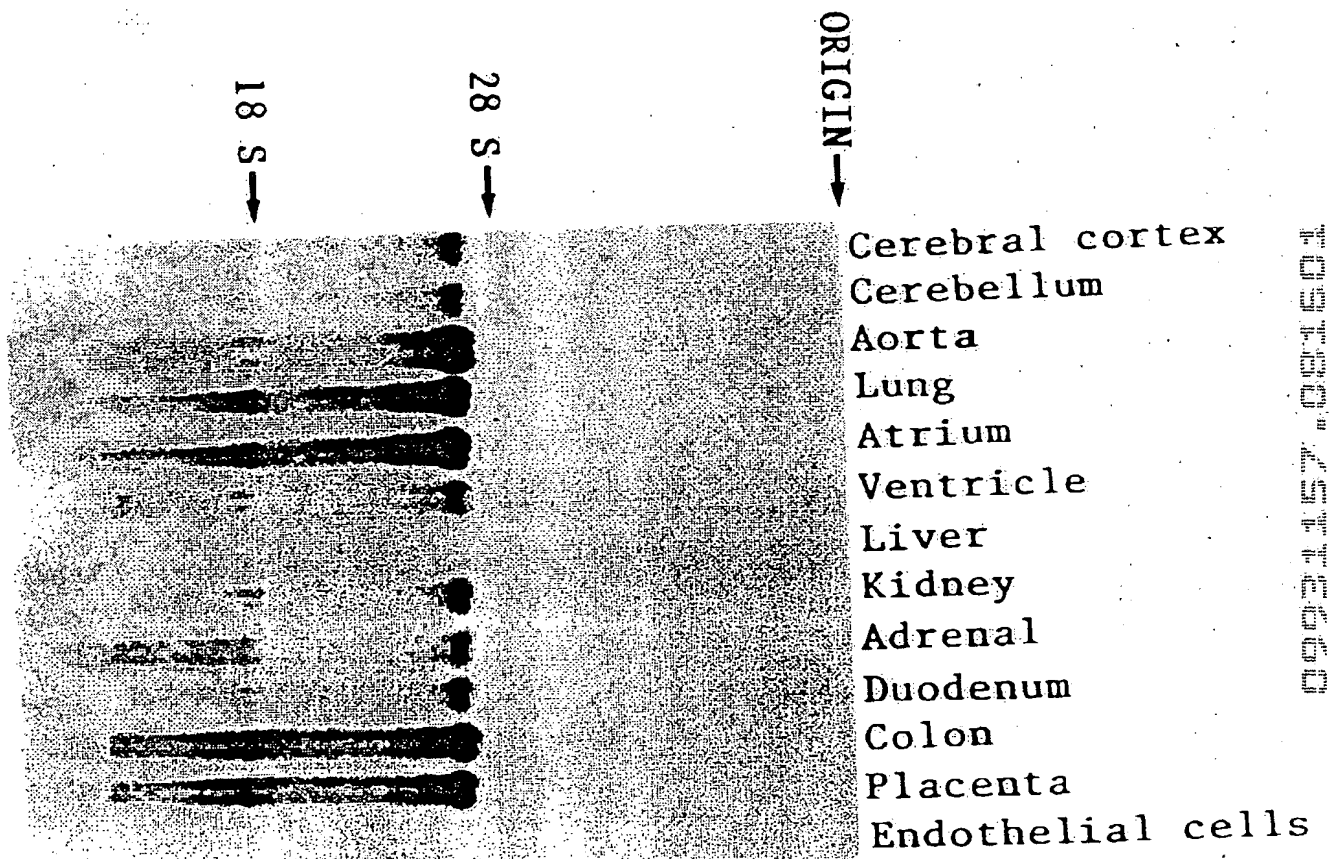


Fig. 6

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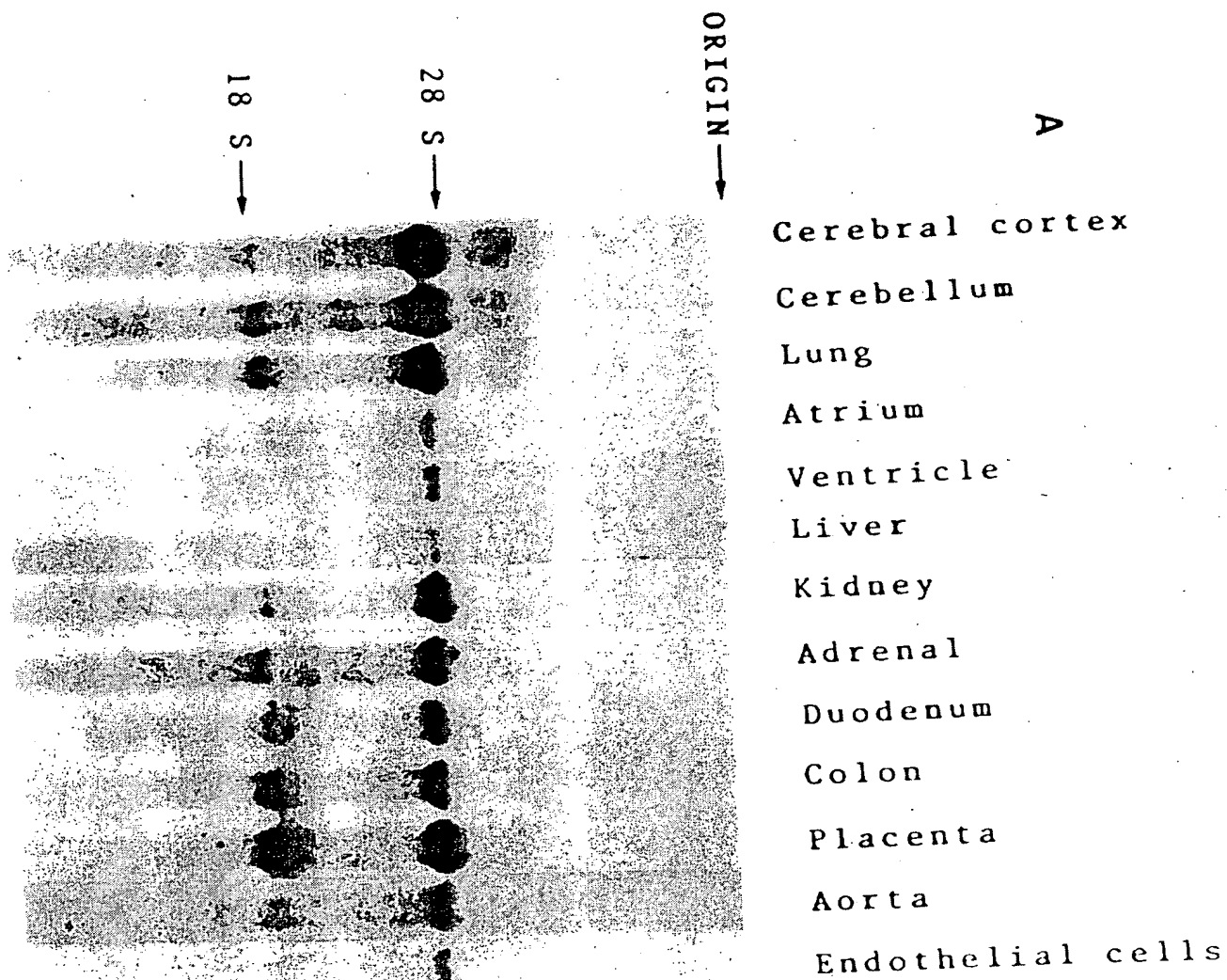


Fig. 7

